

#2

OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/024,955

DATE: 04/16/2002

TIME: 16:20:42

Input Set : N:\Crf3\RULE60\10024955.raw
Output Set: N:\CRF3\04162002\J024955.raw

## SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

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(i) APPLICANT: Wayne R. Thomas and Kaw-Yan Chua
      7
            (ii) TITLE OF INVENTION: Allergenic Proteins and Peptides From
                                      House Dust Mite and Uses Therefor
      8
     10
           (iii) NUMBER OF SEQUENCES: 15
     12
            (iv) CORRESPONDENCE ADDRESS:
     13
                  (A) ADDRESSEE: LAHIVE & COCKFIELD, LLP
     14
                  (B) STREET: 28 State Street
                                                              ENTERED
     15
                  (C) CITY: Boston
                  (D) STATE: Massachusetts
     16
     17
                  (E) COUNTRY: USA
     18
                  (F) ZIP: 02109
             (V) COMPUTER READABLE FORM:
     20
     21
                  (A) MEDIUM TYPE: Floppy disk
     22
                  (B) COMPUTER: IBM PC compatible
     23
                  (C) OPERATING SYSTEM: PC-DOS/MS-DOS
     24
                  (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
     26
            (vi) CURRENT APPLICATION DATA:
                  (A) APPLICATION NUMBER: US/10/024,955
C--> 27
C--> 28
                  (B) FILING DATE: 19-Dec-2001
     29
                  (C) CLASSIFICATION:
     31
           (vii) PRIOR APPLICATION DATA:
     33
                  (A) APPLICATION NUMBER: US/08/553,336A
     34
                  (B) FILING DATE: 10-JUN-1996
     36
                  (A) APPLICATION NUMBER: US 08/081,540
     37
                  (B) FILING DATE: 22-JUNE-1993
     39
          (viii) ATTORNEY/AGENT INFORMATION:
     40
                  (A) NAME: Jane E. Remillard
     41
                  (B) REGISTRATION NUMBER: 38,872
     42
                  (C) REFERENCE/DOCKET NUMBER: IMI-032CP2
     44
            (ix) TELECOMMUNICATION INFORMATION:
     45
                  (A) TELEPHONE: (617)227-7400
     46
                  (B) TELEFAX: (617)742-4214
     49
        (2) INFORMATION FOR SEQ ID NO: 1:
     51
             (i) SEQUENCE CHARACTERISTICS:
     52
                  (A) LENGTH: 812 base pairs
     53
                  (B) TYPE: nucleic acid
     54
                  (C) STRANDEDNESS: single
     55
                  (D) TOPOLOGY: linear
     57
            (ii) MOLECULE TYPE: cDNA
     60
            (ix) FEATURE:
     61
                  (A) NAME/KEY: CDS
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62						ON:	68.	712									
64																	
65	(A) NAME/KEY: mat_peptide																
66	·																
69																	
																CTTTT	60
	TTAC	CAA															109
74				Met	-	Leu	Leu	Leu	Ile		Ala	Ala	Ala	Phe		Ala .	
75			-17		-15					-10					- 5		
	GTT																157
78	Val	Ser	Ala	Asp	Pro	Ile	His	Tyr	Asp	Lys	Ile	Thr	Glu	Glu	Ile	Asn	
79				1				5					10				
81	AAA	GCT	GTT	GAT	GAA	GCC	GTC	GCT	GCA	ATT	GAA	AAA	TCC	GAA	ACA	TTC	205
82	Lys	Ala	Val	Asp	Glu	Ala		Ala	Ala	Ile	Glu	Lys	Ser	Glu	Thr	Phe	
83		15					20					25					
85	GAT	CCA	ATG	AAG	GTA	CCC	GAT	CAT	TCT	GAT	AAA	TTC	GAA	CGA	CAT	ATT	253
86	Asp	Pro	Met	Lys	Val	Pro	Asp	His	Ser	Asp	Lys	Phe	Glu	Arg	His	Ile	
87	30					35					40					45	
89	GGT	ATC	ATC	GAT	TTA	AAA	GGT	GAA	TTA	GAC	ATG	CGA	AAC	ATT	CAA	GTT	301
90	Gly	Ile	Ile	Asp	Leu	Lys	Gly	Glu	Leu	Asp	Met	Arg	Asn	Ile	Gln	Val	
91					50					55					60		
93	CGA	GGA	TTA	AAA	CAA	ATG	AAA	CGT	GTA	GGT	GAT	GCT	AAT	GTG	AAA	AGT	349
94	Arg	Gly	Leu	Lys	Gln	Met	Lys	Arg	Val	Gly	Asp	Ala	Asn	Val	Lys	Ser	•
95				65					70					75			
97	GAA	GAT	GGT	GTT	GTC	AAA	GCT	CAT	TTG	TTG	GTC	GGT	GTT	CAT	GAT	GAC	397
98	Glu	Asp	Gly	Val	Val	Lys	Ala	His	Leu	Leu	Val	Gly	Val	His	Asp	Asp	
99			80					85					90				
101	LGTT	GTT	TCA	ATC	GAA	TAT	' GA'I	TTA	GC	TAC	. AAA	TTC	GGI	' GAT	CTI	CAT	445
102	2 Val	Va]	. Ser	Met	: Glu	Tyr	Asp	Leu	Ala	туг	Lys	Leu	ı Gly	Asp	Leu	His	
103	3	95	5				100	)				105	5				
105	CCA	AAC	CACI	CAT	GTC	ATI	TC	GAT	' ATT	CAC	GAT	TTT	GTI	GTC	GAA	ATT	493
106	Pro	Asr	Thr	His	. Val	Ile	Ser	: Asp	Ile	Glr.	ı Asp	Phe	val	. Val	. Glu	Leu	
107	7 110					115	i				120	)				125	
109	TCG	CTC	GAA	GTI	AGC	GAA	GAA	A GGT	' AAT	' ATG	ACA	TTO	ACA	TCG	TTC	GAA	541
110	Ser	Let	Glu	Val	. Ser	Glu	Glu	ı Gly	Asr	Met	Thr	Leu	Thr	Ser	Phe	Glu	
111	Ļ				130	)		_		135	;				140		
113	GTA	CGT	CAA	TTI	GCC	AAT	GTI	GTC	' AA	CAT	TTA	GGT	GGI	CTI	TCA	ATT	589
114	. Val	Arc	Gln	Phe	. Ala	Asn	Val	. Val	Asr	n His	Ile	Gly	7 Gly	Leu	Ser	· Ile	
115		-	•	145					150			_	_	155			
		GAI	CCA			GCT	GTC	TTA	TCC	GAT	GTT	TTO	ACC	GCI	ATT	TTC	637
																Phe	
119		- 1	160					165					170				
		GAT			CGT	' GCA	GAA	ATG	ACC	: AAA	GTA	TTG	GCA	CCA	GCA	TTC	685
																Phe	
123		175			5		180			1-		185				· <b>-</b>	
	AAA			ттс	GAA	CGA			CAA	TAG	ACTT			ACAT	'AA		732
	Lys																
	190	-	. J_u			195		1-11		-							
			ידידאי	<b>ተ</b> ሞሞ Δ	CACT			CAAA	ጥ ፍል	ΔηΔ	דידאב	י יייי	ΤΥΥΤ	САТ	ጥጥጥር	TTTAAA	792
	CAC	-011				n		14 167									. , , , ,

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131 AAAAAAAAA AAAAAAAAA
                                                                            812
134 (2) INFORMATION FOR SEQ ID NO: 2:
136
         (i) SEQUENCE CHARACTERISTICS:
137
              (A) LENGTH: 215 amino acids
138
              (B) TYPE: amino acid
139
              (D) TOPOLOGY: linear
        (ii) MOLECULE TYPE: protein
141
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145 Met Met Lys Leu Leu Ile Ala Ala Ala Ala Phe Val Ala Val Ser
146 -17
           -15
                                -10
148 Ala Asp Pro Ile His Tyr Asp Lys Ile Thr Glu Glu Ile Asn Lys Ala
149
                                              10
151 Val Asp Glu Ala Val Ala Ala Ile Glu Lys Ser Glu Thr Phe Asp Pro
                     20
                                          25
154 Met Lys Val Pro Asp His Ser Asp Lys Phe Glu Arg His Ile Gly Ile
155
                 35
                                     40
157 Ile Asp Leu Lys Gly Glu Leu Asp Met Arg Asn Ile Gln Val Arg Gly
158
             50
                                 55
160 Leu Lys Gln Met Lys Arg Val Gly Asp Ala Asn Val Lys Ser Glu Asp
                             70
                                                  75 -
163 Gly Val Val Lys Ala His Leu Leu Val Gly Val His Asp Asp Val Val
166 Ser Met Glu Tyr Asp Leu Ala Tyr Lys Leu Gly Asp Leu His Pro Asn
167
                    100
                                         105
169 Thr His Val Ile Ser Asp Ile Gln Asp Phe Val Val Glu Leu Ser Leu
170
                                    120
                115
172 Glu Val Ser Glu Glu Gly Asn Met Thr Leu Thr Ser Phe Glu Val Arg
            130
                                135
175 Gln Phe Ala Asn Val Val Asn His Ile Gly Gly Leu Ser Ile Leu Asp
                            150
                                                 155
178 Pro Ile Phe Ala Val Leu Ser Asp Val Leu Thr Ala Ile Phe Gln Asp
                        165
                                             170
181 Thr Val Arg Ala Glu Met Thr Lys Val Leu Ala Pro Ala Phe Lys Lys
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                    180
                                         185
184 Glu Leu Glu Arg Asn Asn Gln
                195
187 (2) INFORMATION FOR SEQ ID NO: 3:
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              (A) LENGTH: 18 base pairs
              (B) TYPE: nucleic acid
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              (C) STRANDEDNESS: single
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              (D) TOPOLOGY: linear
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        (ii) MOLECULE TYPE: cDNA
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
201 GATCCAATTC ACTATGAT
                                                                             18
203 (2) INFORMATION FOR SEQ ID NO: 4:
         (i) SEQUENCE CHARACTERISTICS:
205
206
              (A) LENGTH: 17 base pairs
207
              (B) TYPE: nucleic acid
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208 (C) STRANDEDNESS: single														
209 (D) TOPOLOGY: linear														
211 (ii) MOLECULE TYPE: CDNA														
215 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:														
217 GGTGAATTAG ACATGCG 219 (2) INFORMATION FOR SEQ ID NO: 5:														
221 (i) SEQUENCE CHARACTERISTICS:														
222 (A) LENGTH: 24 base pairs														
223 (B) TYPE: nucleic acid														
224 (C) STRANDEDNESS: single														
225 (D) TOPOLOGY: linear														
227 (ii) MOLECULE TYPE: cDNA														
231 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:														
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247 (A) NAME/KEY: CDS														
248 (B) LOCATION: 43681														
251 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:														
253 GATCTTATAT CAATAACAAT CCAAAAAAAC ATATCTTACA AA ATG ATG AAA TTT	54													
254 MET MET LVS PNE														
254 Met Met Lys Phe 255 1														
<u>-</u>	102													
255	102													
255 1 257 TTG TTG ATT GCT GCC GTG GCA TTT GTC GCC GTT TCG GCT GAT CCA ATT 258 Leu Leu Ile Ala Ala Val Ala Phe Val Ala Val Ser Ala Asp Pro Ile 259 5 10 15 20	102													
255 1 257 TTG TTG ATT GCT GCC GTG GCA TTT GTC GCC GTT TCG GCT GAT CCA ATT 258 Leu Leu Ile Ala Ala Val Ala Phe Val Ala Val Ser Ala Asp Pro Ile 259 5 10 15 20 261 CAC TAT GAT AAA ATC ACC GAA GAA ATC AAC AAA GCT ATT GAT GAT GCC	102													
255 257 TTG TTG ATT GCT GCC GTG GCA TTT GTC GCC GTT TCG GCT GAT CCA ATT 258 Leu Leu Ile Ala Ala Val Ala Phe Val Ala Val Ser Ala Asp Pro Ile 259 5 10 15 20 261 CAC TAT GAT AAA ATC ACC GAA GAA ATC AAC AAA GCT ATT GAT GAT GCC 262 His Tyr Asp Lys Ile Thr Glu Glu Ile Asn Lys Ala Ile Asp Asp Ala														
255 257 TTG TTG ATT GCT GCC GTG GCA TTT GTC GCC GTT TCG GCT GAT CCA ATT 258 Leu Leu Ile Ala Ala Val Ala Phe Val Ala Val Ser Ala Asp Pro Ile 259 5 10 15 20 261 CAC TAT GAT AAA ATC ACC GAA GAA ATC AAC AAA GCT ATT GAT GAT GCC 262 His Tyr Asp Lys Ile Thr Glu Glu Ile Asn Lys Ala Ile Asp Asp Ala 263 30 35	150													
255 257 TTG TTG ATT GCT GCC GTG GCA TTT GTC GCC GTT TCG GCT GAT CCA ATT 258 Leu Leu Ile Ala Ala Val Ala Phe Val Ala Val Ser Ala Asp Pro Ile 259 5 10 15 20 261 CAC TAT GAT AAA ATC ACC GAA GAA ATC AAC AAA GCT ATT GAT GAT GCC 262 His Tyr Asp Lys Ile Thr Glu Glu Ile Asn Lys Ala Ile Asp Asp Ala 263 25 30 35 265 ATT GCT GCT ATT GAA CAA CAA TCC GAA ACA ATA GAT CCA ATG AAA GTA CCT														
255 257 TTG TTG ATT GCT GCC GTG GCA TTT GTC GCC GTT TCG GCT GAT CCA ATT 258 Leu Leu Ile Ala Ala Val Ala Phe Val Ala Val Ser Ala Asp Pro Ile 259 5 10 15 20 261 CAC TAT GAT AAA ATC ACC GAA GAA ATC AAC AAA GCT ATT GAT GAT GCC 262 His Tyr Asp Lys Ile Thr Glu Glu Ile Asn Lys Ala Ile Asp Asp Ala 263 25 30 35 265 ATT GCT GCT ATT GAA CAA TCC GAA ACA ATA GAT CCA ATG AAA GTA CCT 266 Ile Ala Ala Ile Glu Gln Ser Glu Thr Ile Asp Pro Met Lys Val Pro	150													
255	150 198													
255	150													
255	150 198													
255	150 198 246													
255 TTG TTG ATT GCT GCC GTG GCA TTT GTC GCC GTT TCG GCT GAT CCA ATT 258 Leu Leu Ile Ala Ala Val Ala Phe Val Ala Val Ser Ala Asp Pro Ile 259 5 10 15 20 261 CAC TAT GAT AAA ATC ACC GAA GAA ATC AAC AAA GCT ATT GAT GAT GCC 262 His Tyr Asp Lys Ile Thr Glu Glu Ile Asn Lys Ala Ile Asp Asp Ala 263 25 30 35 265 ATT GCT GCT ATT GAA CAA TCC GAA ACA ATA GAT CCA ATG AAA GTA CCT 266 Ile Ala Ala Ile Glu Gln Ser Glu Thr Ile Asp Pro Met Lys Val Pro 267 40 45 50 269 GAT CAT GCC GAT AAA TTC GAA CGT CAT GTT GGT ATT GTG GAT TTC AAA 270 Asp His Ala Asp Lys Phe Glu Arg His Val Gly Ile Val Asp Phe Lys 271 55 60 65 273 GGT GAA TTA GCC ATG CGA AAC ATT GAG GCT CGA GGA TTG AAA CAA ATG	150 198													
255 TTG TTG ATT GCT GCC GTG GCA TTT GTC GCC GTT TCG GCT GAT CCA ATT 258 Leu Leu Ile Ala Ala Val Ala Phe Val Ala Val Ser Ala Asp Pro Ile 259 5 10 15 20 261 CAC TAT GAT AAA ATC ACC GAA GAA ATC AAC AAA GCT ATT GAT GAT GCC 262 His Tyr Asp Lys Ile Thr Glu Glu Ile Asn Lys Ala Ile Asp Asp Ala 263 25 30 35 265 ATT GCT GCT ATT GAA CAA TCC GAA ACA ATA GAT CCA ATG AAA GTA CCT 266 Ile Ala Ala Ile Glu Gln Ser Glu Thr Ile Asp Pro Met Lys Val Pro 267 40 45 50 269 GAT CAT GCC GAT AAA TTC GAA CGT CAT GTT GGT ATT GTG GAT TTC AAA 270 Asp His Ala Asp Lys Phe Glu Arg His Val Gly Ile Val Asp Phe Lys 271 55 60 65 273 GGT GAA TTA GCC ATG CGA AAC ATT GAG GCT CGA GGA TTG AAA CAA ATG 274 Gly Glu Leu Ala Met Arg Asn Ile Glu Ala Arg Gly Leu Lys Gln Met	150 198 246													
255 TTG TTG ATT GCT GCC GTG GCA TTT GTC GCC GTT TCG GCT GAT CCA ATT 258 Leu Leu Ile Ala Ala Val Ala Phe Val Ala Val Ser Ala Asp Pro Ile 259 5	150 198 246													
255 TTG TTG ATT GCT GCC GTG GCA TTT GTC GCC GTT TCG GCT GAT CCA ATT 258 Leu Leu Ile Ala Ala Val Ala Phe Val Ala Val Ser Ala Asp Pro Ile 259 5	150 198 246 294													
255 TTG TTG ATT GCT GCC GTG GCA TTT GTC GCC GTT TCG GCT GAT CCA ATT 258 Leu Leu Ile Ala Ala Val Ala Phe Val Ala Val Ser Ala Asp Pro Ile 259 5	150 198 246 294													
255 TTG TTG ATT GCT GCC GTG GCA TTT GTC GCC GTT TCG GCT GAT CCA ATT 258 Leu Leu Ile Ala Ala Val Ala Phe Val Ala Val Ser Ala Asp Pro Ile 259 5	150 198 246 294													
255	150 198 246 294													
255 257 TTG TTG ATT GCT GCC GTG GCA TTT GTC GCC GTT TCG GCT GAT CCA ATT 258 Leu Leu Ile Ala Ala Val Ala Phe Val Ala Val Ser Ala Asp Pro Ile 259 5 10 10 15 20 261 CAC TAT GAT AAA ATC ACC GAA GAA ATC AAC AAA GCT ATT GAT GAT GCC 262 His Tyr Asp Lys Ile Thr Glu Glu Ile Asn Lys Ala Ile Asp Asp Ala 263 25 30 35 265 ATT GCT GCT ATT GAA CAA TCC GAA ACA ATA GAT CCA ATG AAA GTA CCT 266 Ile Ala Ala Ile Glu Gln Ser Glu Thr Ile Asp Pro Met Lys Val Pro 267 40 45 50 269 GAT CAT GCC GAT AAA TTC GAA CGT CAT GTT GGT ATT GTG GAT TTC AAA 270 Asp His Ala Asp Lys Phe Glu Arg His Val Gly Ile Val Asp Phe Lys 271 55 60 65 273 GGT GAA TTA GCC ATG CGA AAC ATT GAG GCT CGA GGA TTG AAA CAA ATG 274 Gly Glu Leu Ala Met Arg Asn Ile Glu Ala Arg Gly Leu Lys Gln Met 275 70 70 75 80 277 AAA CGT CAA GGT GAT GCT AAT GTC AAA GGT GAA GAG GGT ATT GTT AAA 278 Lys Arg Gln Gly Asp Ala Asn Val Lys Gly Glu Glu Gly Ile Val Lys 279 85 90 95 100 281 GCT CAT TTG TTG ATC GGT GTT CAC GAT GAT ATC GTC ATG GAA TAT	150 198 246 294													

286 ASP LEU ALB TYP LYS LEU GLY ASP LEU HIS PRO THY THY HAY VAI LE 287 120 125 130 130 125 130 126 127 130 130 128 130 129 130 145 145 145 145 145 145 145 145 145 145	285	САТ	ጥጥል	CCA	<b>ጥ</b> ል C	ααα	ጥጥር	ССТ	СΔТ	Стт	СУП	CCA	ACC	a Cm	СУТ	GTC	<b>Δ</b> ጥጥ	438
287 T. 120																		400
289   TGG GAT ATT CAA GAT TTT GTT GTT GCT TTG TCC CTT GAA ATT TCT GAT   290   Ser Asp 11e Gln Asp Phe Val Val Ala Leu Ser Leu Glu Tle Ser Asp   291   135   140   145		кэр	Deu	ALG	_	כעם	пси	GLY	чэБ		1113	110	1111	1111		Val	116	
990 Ser Asp Ile Gln Asp Phe Val Val Ala Leu Ser Leu Glu Ile Ser Asp 291 135 140 293 GAA GGT AAC ATA ACA ATG ACA TCT TTT GAA GTA CGA CAA TTC GCT AAT 294 Glu Gly Asn Ile Thr Met Thr Ser Phe Glu Val Arg Gln Phe Ala Asn 295 150 150 155 160 297 GTT GTC AAC CAT ATT GGT GGT CTT TCA ATC TTG GAT CAA TTT TTT GGC 298 Val Val Asn His Ile Gly Gly Leu Ser Ile Leu Asp Pro Ile Phe Gly 299 165 170 175 180 301 GTT TTA TCT GAT GTA TTG ACC GCT ATT TCC CAA GAC ACC GTA AGT AGG 302 Val Leu Ser Asp Val Leu Thr Ala Ile Phe Gln Asp Thr Val Arg 303 185 190 195 305 GAA ATG ACC AAA GTA TTG GCA CCA GCA TTT TAAA CCT GAA CAA TT GAA AGA 306 Glu Met Thr Lys Val Leu Ala Pro Ala Phe Lys Arg Glu Leu GaA AAA 678 306 GAA ATA ACCAAAAAA ACATCATTTT TCCAACTGTA CAATCTCTAT TTCACTGACA 307 A20 200 205 210 308 AAT TAACCAAATAA ACATCATTTT TCAACTGTA CAATCTCTAT TTCACTGACA 310 ASS  313 ATAAAAAAAAA ATTTTTATTTTCTCC 761 314 (2) INFORMATION FOR SEQ ID NO: 7: 318 (i) SEQUENCE CHARACTERISTICS: 319 (A) LENGTH: 213 amino acids 320 (B) TYPE: amino acid 321 (D) TOPOLOGY: linear 323 (ii) MOLECULE TYPE: protein 325 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7: 327 Met Met Lys Phe Leu Leu Ile Ala Ala Val Ala Phe Val Ala Val Ser 331 12 Asp Asp Ala Ile Ala Ala Ile Glu Gln Ser Glu Thr Ile Asp Pro 334 12 20 25 30 333 11e Asp Asp Ala Ile Ala Ala Ile Glu Gln Ser Glu Thr Ile Asp Pro 334 12 5		mcc	ርአጥ	א יויייי		СУП	աատ	CTT	CTT		ጥጥር	TCC	СФФ	GNA		ጥርጥ	СЛП	186
291 135 140 145																		400
293 GAA GGT AAC ATA ACA ATG ACA TCT TTT GAA GTA CAC CAA TTC GCT AAT 294 Glu Gly Asn Ile Thr Met Thr Ser Phe Glu Val Arg Gln Phe Ala Asn 295 150 150 160 297 GTT GTC AAC CAT ATT GGT GGT CTT TCA ATC TTG GGT CCA ATT TTT GGC 298 Val Val Asn His Ile Gly Gly Leu Ser Ile Leu Asp Pro Ile Phe Gly 299 165 170 175 180 301 GTT TTA TCT GAT GTA TTG ACC GCT ATT TTC CAA GAC ACC GTA CGT AAG 302 Val Leu Ser Asp Val Leu Thr Ala Ile Phe Gln Asp Thr Val Arg Lys 303 185 190 195 305 GAA ATG ACC AAA GTA TTG GCA CCA GCT ATT AAA CGT GAA ATTG GAA AAA 306 Glu Met Thr Lys Val Leu Ala Pro Ala Phe Lys Arg Glu Leu Glu Lys 307 200 205 210 308 AAT TAACCAATAG ACATCATTTT TCCAACTGTA CAATCTCTAT TTCACTGACA 310 Asn 313 ATAAAATAAA ATTTTTATTTTTTTCC 761 316 (2) INFORMATION FOR SEQ ID NO: 7: 318 (i) SEQUENCE CHARACTERISTICS: 319 (A) LENGTH: 213 amino acids 320 (B) TYPE: amino acids 321 (ii) MOLECULE TYPE: protein 325 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7: 326 (ii) MCLECULE TYPE: protein 327 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7: 330 Ala Asp Pro Ile His Tyr Asp Lys Ile Thr Glu Glu Ile Asn Lys Ala 331 1le Asp Asp Ala Ile Ala Ala Ile Glu Gln Ser Glu Thr Ile Asp Pro 334 35 40 45 35 40 335 40 Asp Phe Lys Gly Glu Leu Ala Met Arg Asn Ile Glu Ala Arg Gly 340 65 70 75 80 341 Asp Pro Lys Gly Glu Leu Ala Met Arg Asn Ile Glu Ala Arg Gly 340 65 70 75 80 341 Asp Pro Lys Ala His Leu Leu Ile Gly Val His Asp Asp Ile Val 343 85 90 95 345 Gly Ile Val Lys Ala His Leu Leu Ile Gly Val His Asp Asp Ile Val 344 Ser Met Glu Tyr Asp Leu Ala Tyr Lys Leu Gly Asp Leu His Pro Thr 349 115 120 355 145 150 135 140 356 Glu Ile Ser Asp Ile Gln Asp Phe Val Val Ala Leu Ser Leu 357 130 130 135 140 358 Glu Ile Ser Asp Ile Gln Asp Phe Val Val Ala Leu Ser Leu 358 110 150 150 155 160		261	тэр		GIII	тэр	riie	Val		AIU	пец	. Jei	пец		TTC	Ser	rsb	
294   Glu Gly Asn Ile Thr Met Thr Ser Phe Glu Val Arg Gln Phe Ala Asn   295   150   155   160   155   160   155   160   155   160   150   160   155   160		CNA	CCT		אידיא	λ C λ	<b>አ</b> ጥር	አሮአ		աատ	CAA	CTIA.	CGA		ጥጥረ	CCT	አአጥ	534
150																		224
297 GTT GTC AAC CAT ATT GGT GGT CTT TCA ATC TTG GAT CCA ATT TTT GGC 298 Val Val Asn His Ile Gly GJT Leu Ser Ile Leu Asp Pro Ile Phe Gly 299 165		GIU	_	изп	TTC	1111	мес		Ser	rne	GIU	Vul	-	GIH	FIIC	AIG	RSII	
298 Val Val Asn His Ile Gly Gly Leu Ser Ile Leu Asp Pro Ile Phe Gly 299 165 170 175 180 301 GTT TTA TCT GAT GTA TTG ACC GCT ATT TTC CAA GAC ACC GTA CGT AAG 302 Val Leu Ser Asp Val Leu Thr Ala Ile Phe Gln Asp Thr Val Arg Lys 303 185 305 GAA ATG ACC AAA GTA TTG GCA CCA GCA TTT AAA CGT GAA TTG GAA AAA 306 Glu Met Thr Lys Val Leu Ala Pro Ala Phe Lys Arg Glu Leu Glu Lys 307 200 205 309 AAT TAACCAATAG ACATCATTTT TCCAACTGTA CAATCTCTAT TTCACTGACA 310 Asn 313 ATAAAATAAA ATTTTTATTT TTATTTCTCC 318 (i) SEQUENCE CHARACTERISTICS: 319 (A) LENGTH: 213 amino acids 320 (B) TYPE: amino acid 321 (D) TOPOLOGY: linear 323 (iii) MOLECULE TYPE: protein 325 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7: 327 Met Met Lys Phe Leu Leu Ile Ala Ala Val Ala Phe Val Ala Val Ser 331 331 Aa Asp Pro Ile His Tyr Asp Lys Ile Thr Glu Glu Ile Asn Lys Ala 331 20 332 333 Ile Asp Asp Ala Ile Ala Ala Ile Glu Gln Ser Glu Thr Ile Asp Pro 334 335 340 350 360 370 380 381 381 380 381 381 380 381 381 381 381 381 381 381 381 381 381		COTO		አአሮ	Слт	ינייני ג	ССТ		CTT	ጥሮል	<b>አ</b> ጥር	ምሞር		CCA	א יייייי א	արա	CCC	582
299 165 170 175 180 301 GTT TTA TCT GAT GTA TTG ACC GCT ATT TTC CAA GAC ACC GTA ACG 302 Val Leu Ser Asp Val Leu Thr Ala 1le Phe Gln Asp Thr Val Arg Lys 303 185 190 195 305 GAA ATG ACC AAA GTA TTG GCA CCA GCA TTT GAA AAA GCT 306 Glu Met Thr Lys Val Leu Ala Pro Ala Phe Lys Arg Glu Leu Glu Lys 307 200 205 210 309 AAT TAACCAATAG ACATCATTT TCCAACTGTA CAATCTCTAT TTCACTGACA 731 300 AAT TAACCAATAG ACATCATTTT TCCAACTGTA CAATCTCTAT TTCACTGACA 731 301 ASD 313 ATAAAATAAA ATTTTTATTT TTATTTCTCC 761 316 (2) INFORMATION FOR SEQ ID NO: 7: 318 (1) SEQUENCE CHARACTERISTICS: 319 (A) LENGTH: 213 amino acids 320 (B) TYPE: amino acid 321 (D) TOPOLOGY: linear 323 (ii) MOLECULE TYPE: protein 325 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7: 326 Met Met Lys Phe Leu Leu Ile Ala Ala Val Ala Phe Val Ala Val Ser 327 Met Met Lys Phe Leu Leu Ile Ala Ala Val Ala Phe Val Ala Val Ser 331 20 25 30 333 Ile Asp Asp Ala Ile Ala Ala Ile Glu Gln Ser Glu Thr Ile Asp Pro 334 35 40 40 45 336 Met Lys Val Pro Asp His Ala Asp Lys Phe Glu Arg His Val Gly Ile 337 50 55 60 339 Val Asp Phe Lys Gly Glu Leu Ala Met Arg Asn Ile Glu Ala Arg Gly 340 65 70 75 80 342 Leu Lys Gln Met Lys Arg Gln Gly Asp Ala Asn Val Lys Gly Glu Glu 343 85 90 95 345 Gly Ile Val Lys Ala His Leu Leu Ile Gly Val His Asp Asp Ile Val 346 100 105 105 348 Ser Met Glu Tyr Asp Leu Ala Tyr Lys Leu Gly Asp Leu His Pro Thr 349 115 120 125 351 Thr His Val Ile Ser Asp Ile Gln Asp Phe Val Val Ala Leu Ser Leu 352 130 135 140 140																		302
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VERIFICATION SUMMARY

DATE: 04/16/2002 TIME: 16:20:43

PATENT APPLICATION: US/10/024,955

Input Set : N:\Crf3\RULE60\10024955.raw Output Set: N:\CRF3\04162002\J024955.raw

L:27 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:] L:28 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]